CLAIMS

What is claimed is:

1. A method of identifying one or more genetic markers for coronary artery disease, wherein each of said one or more genetic markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having coronary artery disease, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for coronary artery disease; and

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals not having coronary artery disease,

wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being genetic markers for coronary artery disease.

2. A method of identifying one or more genetic markers for coronary artery disease, wherein each of said one or more genetic markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having coronary artery disease, wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for coronary artery disease; and

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals having coronary artery disease,

wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being genetic markers for coronary artery disease.

3. A method of identifying one or more genetic markers of a stage of coronary artery disease progression or regression, wherein each of said one or more genetic markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of coronary artery disease, wherein said one or more individuals are at the same progressive or regressive stage of coronary artery disease, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of coronary artery disease, and;

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of coronary artery disease distinct from that of said one or more individuals of step a),

wherein those compared transcripts which display differing levels in the comparison of step b) are identified as being genetic markers for the stage of progression or regression of coronary artery disease.

4. A method of identifying one or more genetic markers of a stage of coronary artery disease progression or regression, wherein each of said one or more genetic markers corresponds to a gene transcript, comprising the steps of:

a) determining the level of one or more gene transcripts expressed in blood obtained from one or more individuals having a stage of coronary artery disease, wherein said one or more individuals are at the same progressive or regressive stage of coronary artery disease, and wherein each of said one or more transcripts is expressed by a gene that is a candidate marker for determining the stage of progression or regression of coronary artery disease, and;

b) comparing the level of each of said one or more gene transcripts from said step a) with the level of each of said one or more genes transcripts in blood obtained from one or more individuals who are at a progressive or regressive stage of coronary artery disease identical to that of said one or more individuals of step a),

wherein those compared transcripts which display the same levels in the comparison of step b) are identified as being genetic markers for the stage of progression or regression of coronary artery disease.

5. The method of any one of claims 1-4, wherein each of said one or more markers identifies one or more transcripts of one or more non immune response genes.

6. The method of any one of claims 1-4, wherein each of said one or more markers identifies a transcript of a gene expressed by non-blood tissue.

7. The method of any one of claims 1-4, wherein each of said one or more markers identifies a transcript of a gene expressed by non-lymphoid tissue.

8. The method of any one of claims 1-4, wherein said one or more markers identifies a sequence selected from the sequences listed in Table 3L.

9. The method of any one of claims 1-4, wherein said one or more markers identifies the sequence of one or more of the sequences selected from the group consisting of ANF, ZFP and MyHC.

10. A method of diagnosing or prognosing coronary artery disease in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts in blood obtained from said individual suspected of having coronary artery disease, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals not having coronary artery disease,

wherein detecting a difference in the levels of each of said one or more gene transcripts in the comparison of step b) is indicative of coronary artery disease in the individual of step a).

11. A method of diagnosing or prognosing coronary artery disease in an individual, comprising the steps of:

a) determining the level of one or more gene transcripts in blood obtained from said individual suspected of having coronary artery disease, and

b) comparing the level of each of said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood from one or more individuals having coronary artery disease,

wherein detecting the same levels of each of said one or more gene transcripts in the comparison of step b) is indicative of coronary artery disease in the individual of step a).

12. A method of determining a stage of disease progression or regression in an individual having coronary artery disease, comprising the steps of:

a) determining the level of one or more gene transcripts in blood obtained from said individual having coronary artery disease, and

b) comparing the level of each if said one or more gene transcripts in said blood according to step a) with the level of each of said one or more gene transcripts in blood obtained from one or more individuals who each have been diagnosed as being at the same progressive or regressive stage of coronary artery disease,

wherein the comparison from step b) allows the determination of the stage of coronary artery disease progression or regression in an individual.

13. The method of any one of claims 1-4 and 10-12, wherein said one or more gene transcripts are transcribed from one or more genes selected from the group consisting of : a) non-immune response genes, b) genes expressed by non blood tissue, and c) genes expressed by non lymphoid tissue.

14. The method of any one of claims 1-4 and 10-12, wherein said blood comprises a blood sample obtained from said one or more individuals.

15. The method of claim 14, wherein said blood sample consists of whole blood.

16. The method of claim 14, wherein said blood sample consists of a drop of blood.

17. The method of claim 14, wherein said blood sample consists of blood that has been lysed.

18. The method of claim 14, further comprising the step of isolating RNA from said blood samples.

19. The method of any one of claims 1-4 and 10-12,wherein the step of determining the level of each of said one or more gene transcripts comprises quantitative RT-PCR (QRT-PCR), wherein said one or more transcripts are from step a) and/or step b) of claims 1-4 and 10-12.

20. The method of claim 19, wherein said QRT-PCR comprises primers which hybridize to said one or more transcripts or the complement thereof, wherein said one or more transcripts are from step a) and/or step b) of claims 1-4 and 10-12.

21. The method of claim 20, wherein said primers are 15-25 nucleotides in length.

22. The method of claim 20, wherein said primers hybridize to one or more of the sequences of Table 3L, or the complement thereof.

23. The method of any one of claims1-4 and 10-12, wherein the step of determining the level of each of said one or more gene transcripts comprises hybridizing a first plurality of isolated nucleic acid molecules that correspond to said one or more transcripts, to an array comprising a second plurality of isolated nucleic acid molecules.

24. The method of claim 23, wherein said first plurality of isolated nucleic acid molecules comprises RNA, DNA, cDNA, PCR products or ESTs.

25. The method of claim 23, wherein said array comprises a plurality of isolated nucleic acid molecules comprising RNA, DNA, cDNA, PCR products or ESTs.

26. The method of claim 25, wherein said array comprises two or more of the genetic markers of claim 1.

27. The method of claim 25, wherein said array comprises two or more of the genetic markers of claim 2.

28. The method of claim 25, wherein said array comprises two or more of the genetic markers of claim 3.

29. The method of claim 25, wherein said array comprises two or more of the genetic markers of claim 4.

30. The method of claim 25, wherein said array comprises a plurality of nucleic acid molecules that correspond to genes of the human genome.

31. The method of claim 25, wherein said array comprises a plurality of nucleic acid molecules that correspond to two or more sequences from Table 3L.

32. A plurality of isolated nucleic acid molecules that correspond to two or more of the genetic markers of claim 1.

33. A plurality of isolated nucleic acid molecules that correspond to two or more of the genetic markers of claim 2.

34. A plurality of isolated nucleic acid molecules that correspond to two or more of the genetic markers of claim 3.

35. A plurality of isolated nucleic acid molecules that correspond to two or more of the genetic markers of claim 4.

36. The method of claim 24 or 25, wherein said ESTs comprise a length from 50-300 nucleotides.

37. An array consisting essentially of the plurality of nucleic acid molecules of claim 32.

38. An array consisting essentially of the plurality of nucleic acid molecules of claim 33.

39. An array consisting essentially of the plurality of nucleic acid molecules of claim 34.

40. An array consisting essentially of the plurality of nucleic acid molecules of claim 35.

41. A kit for diagnosing or prognosing coronary artery disease comprising: a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene selected from the group consisting of Table 3L; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product; b) an enzyme with reverse transcriptase activity c) an enzyme with thermostable DNA polymerase activity and d) a labeling means; wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

42. A kit for monitoring a course of therapeutic treatment of coronary artery disease, comprising a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene selected group consisting of Table 3L; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product; b) an enzyme with reverse transcriptase activity c) an

enzyme with thermostable DNA polymerase activity and d) a labeling means; wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

43. A kit for monitoring progression or regressionof coronary artery disease, comprising: a) two gene-specific priming means designed to produce double stranded DNA complementary to a gene selected group consisting of Table 3L; wherein said first priming means contains a sequence which can hybridize to RNA, cDNA or an EST complementary to said gene to create an extension product and said second priming means capable of hybridizing to said extension product; b) an enzyme with reverse transcriptase activity c) an enzyme with thermostable DNA polymerase activity and d) a labeling means; wherein said primers are used to detect the quantitative expression levels of said gene in a test subject.

44. A plurality of nucleic acid molecules that identify or correspond to two or more sequences from Table 3L.